

SEQUENCE LISTING

<110> Goldman, Stanley
Lathrop, Stephanie
Longchamp, Pascal
Whalen, Robert

<120> Methods and Compositions for Developing
Spore Display Systems for Medicinal and Industrial
Applications

<130> 43432/234498

<150> US 60/214,161

<151> 2000-06-26

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 258

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)...(258)

<223> CotC27 including HA11 region

<400> 1

atg	ggt	tat	tac	aaa	aaa	tac	aaa	gaa	gag	tat	tat	acg	gtc	aaa	aaa	48
Met	Gly	Tyr	Tyr	Lys	Lys	Tyr	Lys	Glu	Glu	Tyr	Tyr	Thr	Val	Lys	Lys	
1				5				10					15			

acg	tat	tat	aag	aag	tat	tac	gaa	tat	gat	aaa	tct	aga	ggt	acc	tgc	96
Thr	Tyr	Tyr	Lys	Lys	Tyr	Tyr	Glu	Tyr	Asp	Lys	Ser	Arg	Gly	Thr	Cys	
			20				25						30			

tat	cct	tat	gat	gtt	cct	gat	tat	gct	tct	tta	gga	tcc	ctg	cag	aaa	144
Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Ser	Leu	Gly	Ser	Leu	Gln	Lys	
		35				40					45					

gat	tat	gac	tgt	gat	tac	gac	aaa	aaa	tat	gat	gac	tat	gat	aaa	aaa	192
Asp	Tyr	Asp	Cys	Asp	Tyr	Asp	Lys	Lys	Tyr	Asp	Asp	Tyr	Asp	Lys	Lys	
	50					55				60						

tat	tat	gat	cac	gat	aaa	aaa	gac	tat	gat	tat	gtt	gta	gag	tat	aaa	240
Tyr	Tyr	Asp	His	Asp	Lys	Lys	Asp	Tyr	Asp	Tyr	Val	Val	Glu	Tyr	Lys	
65					70				75						80	

aag	cat	aaa	aaa	cac	tac											258
Lys	His	Lys	Lys	His	Tyr											
				85												

<210> 2
 <211> 639
 <212> DNA
 <213> Bacillus circulans

<220>
 <221> CDS
 <222> (1)...(639)
 <223> lipase 396

<400> 2
 atg aaa ttt ata aaa aga agg atc att gca ctt gta aca att ttg gtg 48
 Met Lys Phe Ile Lys Arg Arg Ile Ile Ala Leu Val Thr Ile Leu Val
 1 5 10 15
 ctg tca gtc aca tcg ctg ttt gcg atg cag ccg tca gca aaa gcc gct 96
 Leu Ser Val Thr Ser Leu Phe Ala Met Gln Pro Ser Ala Lys Ala Ala
 20 25 30
 gaa cac aat cca gtt gtt atg gtt cac ggt atc gga gga gct tca tac 144
 Glu His Asn Pro Val Val Met Val His Gly Ile Gly Gly Ala Ser Tyr
 35 40 45
 aat ttt gcg gga att aag agc tat ctc gta tct cag ggc tgg tca cgg 192
 Asn Phe Ala Gly Ile Lys Ser Tyr Leu Val Ser Gln Gly Trp Ser Arg
 50 55 60
 ggc aag ctg tat gcg gtt gat ttt tgg gac aag aca ggg acg aat tat 240
 Gly Lys Leu Tyr Ala Val Asp Phe Trp Asp Lys Thr Gly Thr Asn Tyr
 65 70 75 80
 aac aat ggc ccg gta tta tca cga ttt gtg caa aag gtt tta gac gaa 288
 Asn Asn Gly Pro Val Leu Ser Arg Phe Val Gln Lys Val Leu Asp Glu
 85 90 95
 acg ggt gcg aaa aaa gtg gat att gtc gct cac agc atg ggt ggc gcg 336
 Thr Gly Ala Lys Lys Val Asp Ile Val Ala His Ser Met Gly Gly Ala
 100 105 110
 aac aca ctt tac tac ata aaa aat ctg gac ggc gga aat aaa att gaa 384
 Asn Thr Leu Tyr Tyr Ile Lys Asn Leu Asp Gly Gly Asn Lys Ile Glu
 115 120 125
 aac gtc gta acg ctt ggc ggc gcg aac cgt ttg acg aca agc aag gcg 432
 Asn Val Val Thr Leu Gly Gly Ala Asn Arg Leu Thr Thr Ser Lys Ala
 130 135 140
 ctt ccg gga aca gat cca aat caa aag att tta tac aca tcc att tac 480
 Leu Pro Gly Thr Asp Pro Asn Gln Lys Ile Leu Tyr Thr Ser Ile Tyr
 145 150 155 160
 agc agt gcc gat atg att gtc atg aat tac tta tca aaa tta gac ggt 528
 Ser Ser Ala Asp Met Ile Val Met Asn Tyr Leu Ser Lys Leu Asp Gly
 165 170 175
 gct aaa aac gtt caa att cat ggc gtt ggg cac att ggt tta ttg atg 576
 Ala Lys Asn Val Gln Ile His Gly Val Gly His Ile Gly Leu Leu Met

180	185	190	
aac agc caa gtc aac agc ctg att aaa gaa gga ctg aac ggc ggg ggc			624
Asn Ser Gln Val Asn Ser Leu Ile Lys Glu Gly Leu Asn Gly Gly Gly			
195	200	205	

ctc aat aca aat taa	639
Leu Asn Thr Asn *	
210	

<210> 3
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer for fusion protein

<400> 3	
atatctgcag atttgtattg aggcccccg	29

<210> 4
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer for terminator

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atatctgcag ttaatttgta ttgaggcccc cg	32